

LL1VH

001.1505876.1

LL1VK

[illegible][illegible]

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 270
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 80
 S G V P D R F S G S G T D F T L K I S R V E A E D L G L
 50 70

337

TAATTTCTGCTCTCAAGTTCACATGTTCTTCTCCACGTTGGTGTGGAGCCAAAGCTGGADATCTAAC
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----
ATTAAGACGAGAGTTTCAAGTGTACACAGAGGAGGTGCAAGCCACGACCTGTGTTGCAACCTTGATTG
30 100
Y F C S Q S S H V P P T F G A G T K L E I
CDR3

Figure 2A

cLL1VH

CAGGTCCAACTGGCAG^{PstI}CTGTGACCTGACCTGAGAGACCTGAGAGACAGTCAAGTCACTGCAAGACTTCTGATATACCTTCACA
 GTCCAGCTT^{BamHI}GACCTGACAGCTGAGCTGACCTTCTTGACCTCTCTGACAGTTCCAGTGGACAGCTTCTGAAGACTATATGAGAGTGT
 Q V Q L Q Q S G P E L K K P G E T V K V T C K T S G Y T F T 30
 AACTATGAGTGAATGATTAAGACAGACTCCAGAGAGGGTTTACAGTGGATGGCTGATTAACCCCAACACTGAGAGCCAAATTT
 TTGATACCTCACTTGACCTAATTCGTGAGGTCCTCTCCCAATGTCACCTACCGACCTAATTTGGGGTTGTAACCTCTCGGTGTAA
 N Y G V N W I K Q T P G B G L Q W M G M I N P N T G E P T F 59
 CDR1 CDR2
 GATGATGACTTCAAGGACGATTTGCTTCTCTTTGGAAATCCTCTGCCAGCACTGCTTTTTCAGATCAGCAACTCAAAATATGAGAC
 CTACTACTGAAGTCCCTGCTTAACGAGAAACCTTAGGAGACGGTCTGACGAAATAAGTCTAGTGGAGTTTACTCCTG 270
 D D D F K G R F A F S L E S S A S T A F L Q I S N L K N E D 89
 ATGGTACATATTTCTGTTCAAGATGAGGGTAAAGAGAGCTGTGTTGCTTATGAGGCAAGGACTCTGTACACCTTCTCTCA
 TACCATGATATAAGACAGTCTAGCTCCCATTTTGTCTTGGACCAAGATTAACCCCGTTCCCTGAGACCAAGTGCAGAGAGT
 M G T Y F C S R S R G K N E A W F A Y W G Q G T L V T V S S 113
 CDR3

Figure 2B

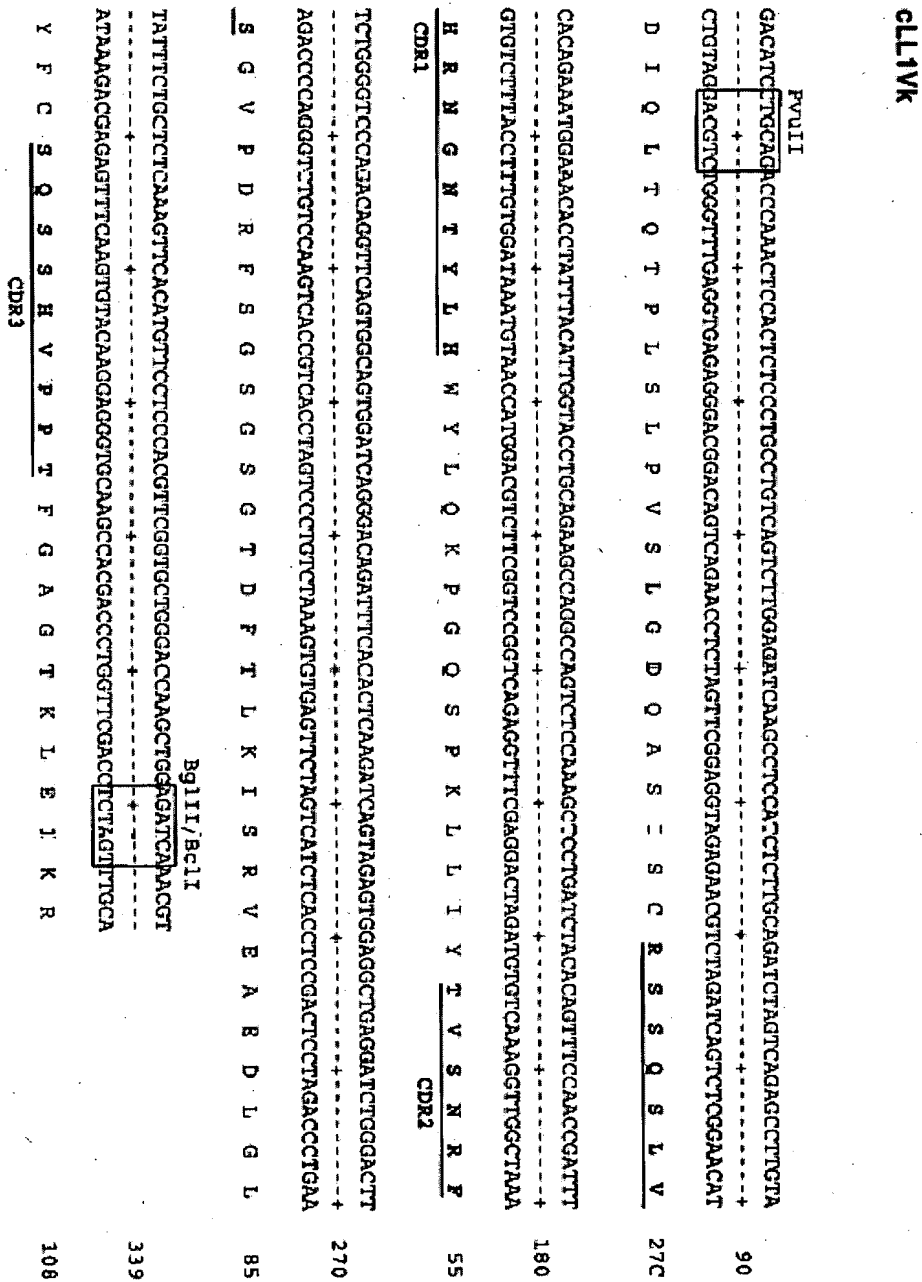


Figure 3A

RF-TS3	QVQLVQSGSELKPGASVKVSCKASGYTFTSYAMN	40
CLL1VH	QVQLQ...P...ET...T...T...N...GV...IK...T	40
hLL1VH	QVQLQ...N...GV...IK...	40
RF-TS3	PGQGLEWMGWINTNTGNTPTYAQGFTGRFVFSLDTSVSTAY	79
CLL1VH	...E...Q...P...E...FDD...A...ES...A...F	79
hLL1VH	...Q...P...E...FDD...A...	79
RF-TS3	LQISSLKADDTAVYYCAR	102
CLL1VH	...N...NE...MGT...F...S...SRGKNEAW...A...	102
hLL1VH	...F...S...SRGKNEAW...A...	102
NEWM	WGQGS�VTVSS	113
CLL1VH	...T...TVSS	113
hLL1VH	...TVSS	113

Figure 3B

HF-21/28	DVMTQSP LSLPVT LGQPASIS	CRSSQSLVHSDGNTYLNW	35
CLL1VK	DIQLT.....S	DQ.....RN.....H	35
hLL1VK	<u>DIQL</u>	<u>.....RN.....H</u>	35

HF-21/28	FQQRPGQSP RRLTYKVS	NRD SGVPDR FSGSGGTDTLKI	75
CLL1VK	YL.....KL.....T.....F.....		75
hLL1VKL.....T.....F.....		75

HF-21/28	SRVEAEDVGVYCMQ	GTHTPFTFGQTRLEI	106
CLL1VKL.....F.....S.....S.....V.....P.....A.....K.....IKR		108
hLL1VKF.....S.....S.....S.....V.....P.....A.....IKR		108

MLL1VH

001.1505876.1

Figure 4B

hLL1VK

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GACATCCAGTCACTCAAGTCTCCACTCTCCCTGCCCGTCAACCTTGGACAGCCGGCTTCATCTCTCGAGATCAAGTCAGAGCCTTGTAA
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CTGTAGGTGCACTGAGTCAAGAGGTGAGAGCGGACCGGCACTGGAACTGTGGCCGGAGGTAGAGACCGTCTAGTTCAGTCTCGGACACAT
D I Q L T Q S P L S L P V T L G Q P A S : S C R S S Q S L V 28C

CACAGAAATGGAACACTATTTACATTTGTTTCAGCAGAGGCCAGGCCAATCTCCAAAGCTCTCTGATCTACACAGTTTCCAAACGATTT
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
GTGTCTTACCTTGTGATTAATGTAAACCAAGTGTCTCCGGTCCGTTAGAGTTCCGAGACTAGATGTGTCAAGGTTGGCTAAA 180

H R N G N T Y L H W F Q Q R P G Q S P R L L I Y T V S N R F 55
CDR1 CDR2

TCGTGGGTCCCAACAGATTTACGCCGCGAGTGGTCAAGCACTGATTTACACTGAATAATCAGCAGGGTGGAGGCTGAGAGATGTTGGGTTT
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
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270

S G V P D R F S G S G S G T D P T L K I S R V E A B D V G V 85

TATTTCTGCTCTTAAGTTACATGTTCTCCCAAGTTGCGTGTGGACACGACTGAGATCAAAAGT
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
ATTAAGACGAGAGTTTCAAGTGTACAGAGAGGGTGCAGGCCACGACCCTGTGCTGACCTCTAGTTTGA 339

Y F C S Q S S H V P P T F G A G T R L E I K R 108
CDR3

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Figure 5

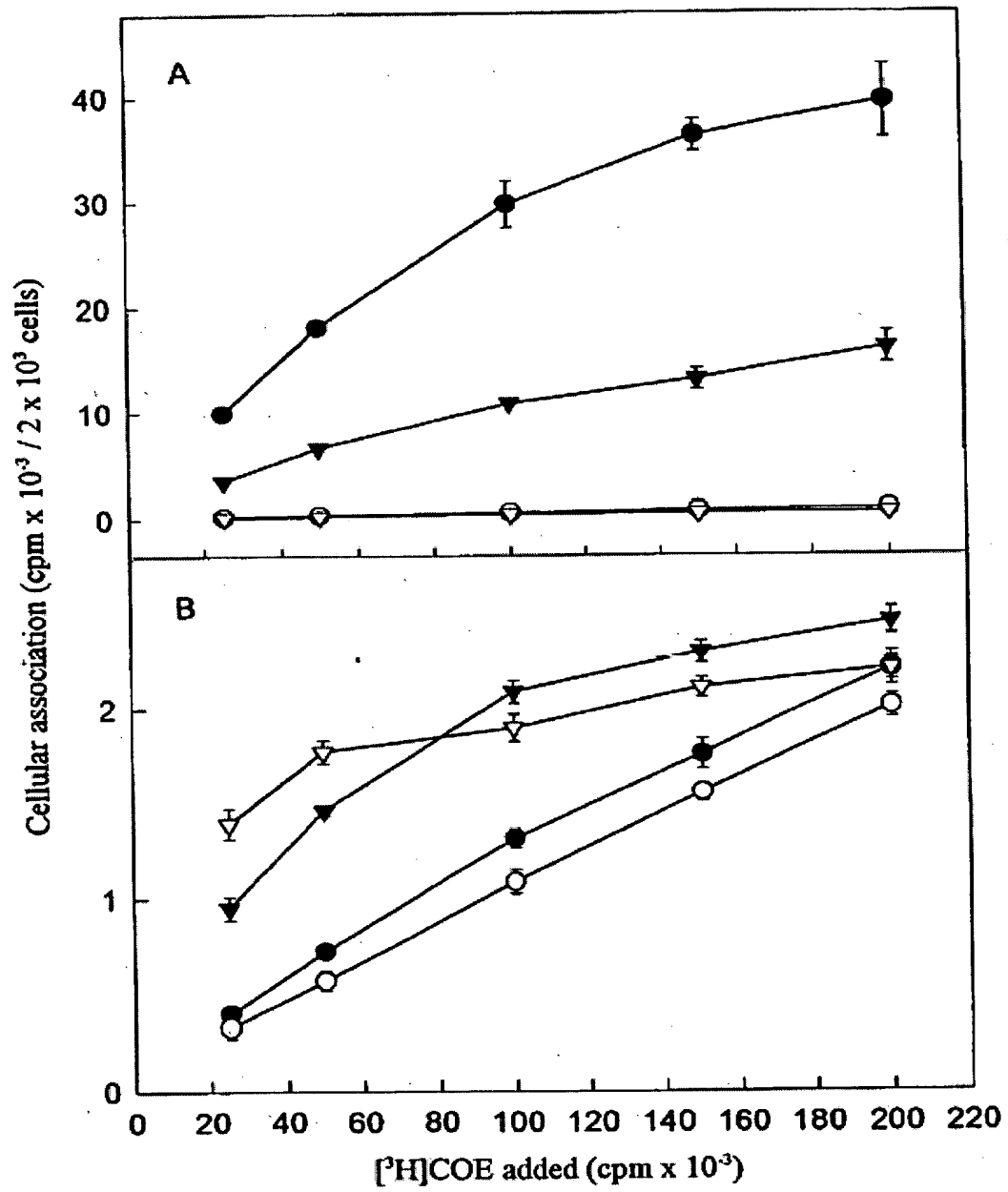


Figure 6

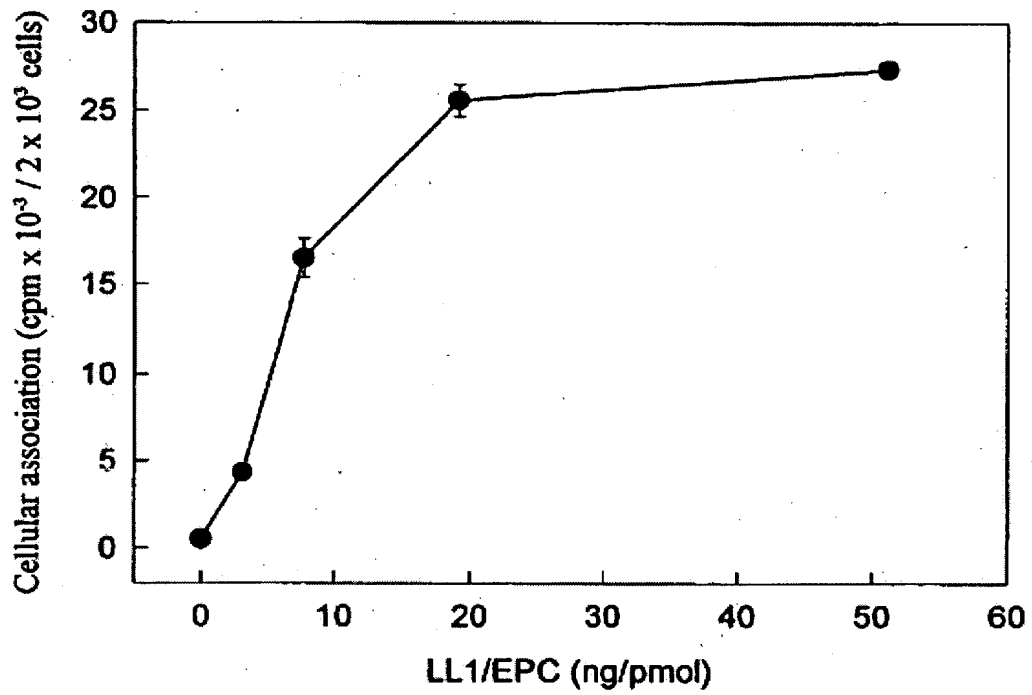


Figure 7

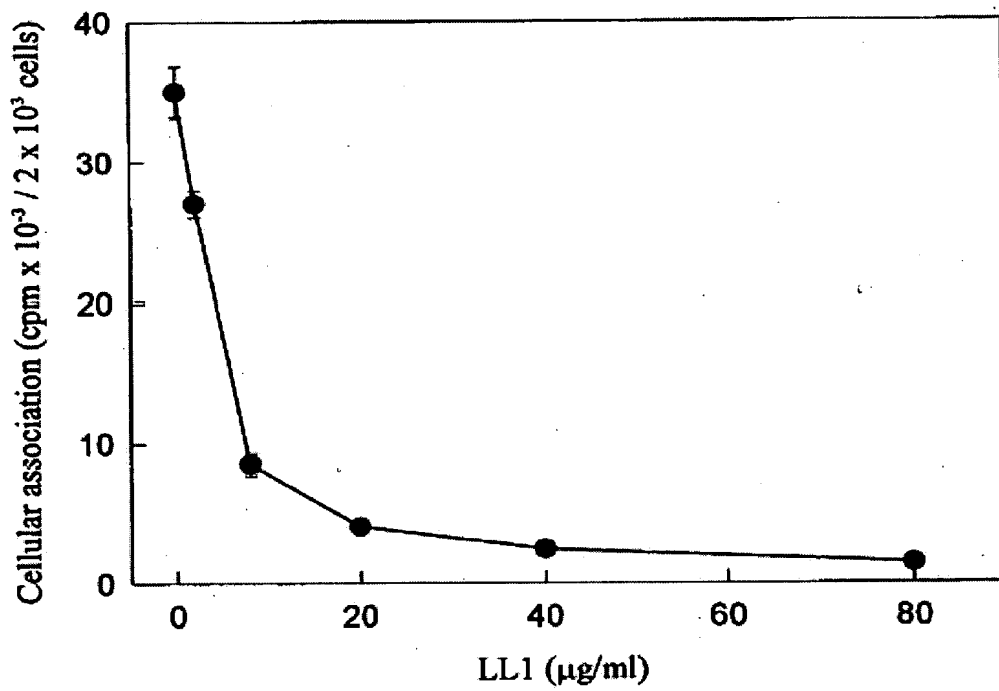


Figure 8

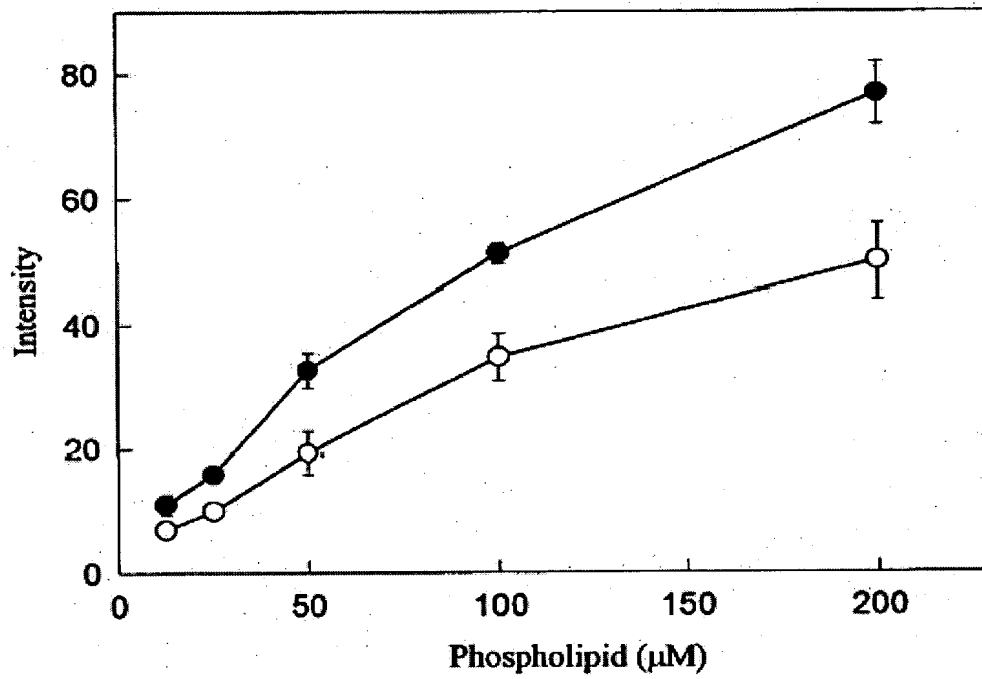


Figure 9

